SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT: DIXIT, VISHVA M.
O'ROURKE, KAREN

(ii) TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR REGULATING FAS-ASSOCIATED APOPTOSIS

(iii) NUMBER OF SEQUENCES: 10

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Morrison & Foerster
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(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

B' cont'd

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/443,982
(B) FILING DATE: 18-MAY-1995
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Konski, Antoinette F.
(B) REGISTRATION NUMBER: 34,202
(C) REFERENCE/DOCKET NUMBER: 20344-21070.20

(ix) TELECOMMUNICATION INFORMATION:
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(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1642 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS

(B) LOCATION: 130..756

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 4..6
(D) OTHER INFORMATION: /note= "An in-frame stop codon 130 base pairs upstream of the initiator methionine"

(ix) FEATURE:
(A) NAME/KEY: polyA_signal
(B) LOCATION: 1636..1641
(D) OTHER INFORMATION: /note= "Potential poly(A) adenylation signal"

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 198..753
(D) OTHER INFORMATION: /note= "Clone-15; 5' end of FADD"

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 249..753
(D) OTHER INFORMATION: /note= "Clone-8; 5' end of FADD"

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 177..658
(D) OTHER INFORMATION: /note= "Death Domain of FADD"

(ix) FEATURE:
(A) NAME/KEY: mutation
(B) LOCATION: replace(490..492, "aay")
(D) OTHER INFORMATION: /note= "For FADDmt: sequence is altered to either AAT or AAC and
the codon from Val to Asn"

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: group(250..753, 232..753)
(D) OTHER INFORMATION: /note= "Codons can comprise C-terminal polypeptide fragments of FADD"

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 253..753
(D) OTHER INFORMATION: /note= "Codons can comprise polypeptide fragment of FADD designated NFD-2"

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 310..753
(D) OTHER INFORMATION: /note= "Codons can comprise polypeptide fragment of FADD designated NFD-3"

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 367..753
(D) OTHER INFORMATION: /note= "Codons can comprise polypeptide fragment of FADD designated NFD-4"

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 131..504
(D) OTHER INFORMATION: /note= "Codons can comprise an N-terminal half polypeptide fragment of FADD designated N-FADD"

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION: 133..501
(D) OTHER INFORMATION: /note= "Codons can comprise an N-terminal half polypeptide fragment of FADD"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
CTCTAAAGGT TCGGGGGTGG AATCCTTGGG CCGCTGGGCA AGCGGCGAGA CCTGGCCAGG      60

GCCAGCGAGC CGAGGACAGA GGGCGCACGG AGGGCCGGGC CGCAGCCCCG GCCGCTTGCA     120

GACCCCGCC ATG GAC CCG TTC CTG GTG CTG CTG CAC TCG GTG TCG TCC          168
          Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser
            1               5                  10

AGC CTG TCG AGC AGC GAG CTG ACC GAG CTC AAG TTC CTA TGC CTC GGG       216
Ser Leu Ser Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly
     15                  20                  25

CGC GTG GGC AAG CGC AAG CTG GAG CGC GTG CAG AGC GGC CTA GAC CTC       264
Arg Val Gly Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu
 30                  35                  40                  45

TTC TCC ATG CTG CTG GAG CAG AAC GAC CTG GAG CCC GGG CAC ACC GAG       312
Phe Ser Met Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu
                 50                  55                  60

CTC CTG CGC GAG CTG CTC GCC TCC CTG CGG CGC CAC GAC CTG CTG CGG       360
Leu Leu Arg Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg
             65                  70                  75

CGC GTC GAC GAC TTC GAG GCG GGG GCG GCG GCC GGG GCC GCG CCT GGG       408
Arg Val Asp Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly
         80                  85                  90

GAA GAA GAC CTG TGT GCA GCA TTT AAC GTC ATA TGT GAT AAT GTG GGG       456
Glu Glu Asp Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly
     95                  100                 105
```

```
AAA GAT TGG AGA AGG CTG GCT CGT CAG CTC AAA GTC TCA GAC ACC AAG       504
Lys Asp Trp Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys
110                 115                 120                 125

ATC GAC AGC ATC GAG GAC AGA TAC CCC CGC AAC CTG ACA GAG CGT GTG       552
Ile Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val
                130                 135                 140

CGG GAG TCA CTG AGA ATC TGG AAG AAC ACA GAG AAG GAG AAC GCA ACA       600
Arg Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr
            145                 150                 155

GTG GCC CAC CTG GTG GGG GCT CTC AGG TCC TGC CAG ATG AAC CTG GTG       648
Val Ala His Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val
        160                 165                 170

GCT GAC CTG GTA CAA GAG GTT CAG CAG GCC CGT GAC CTC CAG AAC AGG       696
Ala Asp Leu Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg
    175                 180                 185

AGT GGG GCC ATG TCC CCG ATG TCA TGG AAC TCA GAC GCA TCT ACC TCC       744
Ser Gly Ala Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser
190                 195                 200                 205

GAA GCG TCC TGA TGGGCCGCTG CTTTGCGCTG GTGGACCACA GGCATCTACA           796
Glu Ala Ser  *

CAGCCTGGAC TTTGGTTCTC TCCAGGAAGG TAGCCCAGCA CTGTGAAGAC CCAGCAGGAA     856

GCCAGGCTGA GTGAGCCACA GACCACCTGC TTCTGAACTC AAGCTGCGTT TATTAATGCC     916

TCTCCCGCAC CAGGCCGGGC TTGGGCCCTG CACAGATATT TCCATTTCTT CCTCACTATG     976

ACACTGAGCA AGATCTTGTC TCCACTAAAT GAGCTCCTGC GGGAGTAGTT GGAAAGTTGG    1036

AACCGTGTCC AGCACAGAAG GAATCTGTGC AGATGAGCAG TCACACTGTT ACTCCACAGC    1096

GGAGGAGACC AGCTCAGAGG CCCAGGAATC GGAGCGAAGC AGAGAGGTGG AGAACTGGGA    1156

TTTGAACCCC CGCCATCCTT CACCAGAGCC CATGCTCAAC CACTGTGGCG TTCTGCTGCC    1216

CCTGCAGTTG GCAGAAAGGA TGTTTTGTCC CATTTCCTTG GAGGCCACCG GGACAGACCT    1276

GGACACTAGG GTCAGGCGGG GTGCTGTGGT GGGGAGAGGC ATGGCTGGGG TGGGGGTGGG    1336

GAGACCTGGT TGGCCGTGGT CCAGCTCTTG GCCCCTGTGT GAGTTGAGTC TCCTCTCTGA    1396

GACTGCTAAG TAGGGGCAGT GATGGTTGCC AGGACGAATT GAGATAATAT CTGTGAGGTG    1456

CTGATGAGTG ATTGACACAC AGCACTCTCT AAATCTTCCT TGTGAGGATT ATGGGTCCTG    1516

CAATTCTACA GTTTCTTACT GTTTTGTATC AAAATCACTA TCTTTCTGAT AACAGAATTG    1576
```

CCAAGGCAGC GGGATCTCGT ATCTTTAAAA AGCAGTCCTC TTATTCCTAA GGTAATCCTA 1636

TTAAAA 1642

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 209 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Asp Pro Phe Leu Val Leu Leu His Ser Val Ser Ser Ser Leu Ser
1 5 10 15

Ser Ser Glu Leu Thr Glu Leu Lys Phe Leu Cys Leu Gly Arg Val Gly
20 25 30

Lys Arg Lys Leu Glu Arg Val Gln Ser Gly Leu Asp Leu Phe Ser Met
35 40 45

Leu Leu Glu Gln Asn Asp Leu Glu Pro Gly His Thr Glu Leu Leu Arg
50 55 60

Glu Leu Leu Ala Ser Leu Arg Arg His Asp Leu Leu Arg Arg Val Asp
65 70 75 80

Asp Phe Glu Ala Gly Ala Ala Ala Gly Ala Ala Pro Gly Glu Glu Asp
85 90 95

Leu Cys Ala Ala Phe Asn Val Ile Cys Asp Asn Val Gly Lys Asp Trp
100 105 110

Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile Asp Ser
115 120 125

Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg Glu Ser
130 135 140

Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val Ala His
145 150 155 160

Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala Asp Leu
165 170 175

Val Gln Glu Val Gln Gln Ala Arg Asp Leu Gln Asn Arg Ser Gly Ala
180 185 190

Met Ser Pro Met Ser Trp Asn Ser Asp Ala Ser Thr Ser Glu Ala Ser
195 200 205

*

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 11
(D) OTHER INFORMATION: /note= "Val is replaced by Asn for the point mutant hFADD"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
Asp Trp Arg Arg Leu Ala Arg Gln Leu Lys Val Ser Asp Thr Lys Ile
1               5                  10                  15

Asp Ser Ile Glu Asp Arg Tyr Pro Arg Asn Leu Thr Glu Arg Val Arg
            20                  25                  30

Glu Ser Leu Arg Ile Trp Lys Asn Thr Glu Lys Glu Asn Ala Thr Val
        35                  40                  45

Ala His Leu Val Gly Ala Leu Arg Ser Cys Gln Met Asn Leu Val Ala
    50                  55                  60

Asp Leu Val Gln Glu Val
65                  70
```

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 11
(D) OTHER INFORMATION: /note= "Ile is replaced by Asn for the point mutant rFas"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Asp Ala Lys Lys Phe Ala Arg Gln His Lys Ile Pro Glu Ser Lys Ile
1               5                  10                  15

Asp Glu Ile Glu His Asn Ser Pro Gln Asp Ala Ala Glu Gln Lys Ile
            20                  25                  30

Gln Leu Leu Gln Cys Trp Tyr Gln Ser His Gly Lys Thr Gly Ala Cys
        35                  40                  45

Gln Ala Leu Ile Gln Gly Leu Arg Lys Ala Asn Arg Cys Asp Ile Ala
    50                  55                  60

Glu Glu Ile Gln Ala Met
65                  70
```

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 11
(D) OTHER INFORMATION: /note= "Val is replaced by Asn for the point mutant hFas"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
Gln Val Lys Gly Phe Val Arg Lys Asn Gly Val Asn Glu Ala Lys Ile
1               5                  10                  15

Asp Glu Ile Lys Asn Asp Asn Val Gln Asp Thr Ala Glu Gln Lys Val
            20                  25                  30

Gln Leu Leu Arg Asn Trp His Gln Leu His Gly Lys Lys Glu Ala Tyr
        35                  40                  45

Asp Thr Leu Ile Lys Asp Leu Lys Lys Ala Asn Leu Cys Thr Leu Ala
    50                  55                  60

Glu Lys Ile Gln Thr Ile
65                  70
```

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 70 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:
(A) NAME/KEY: Modified-site
(B) LOCATION: 11
(D) OTHER INFORMATION: /note= "Leu is replaced by Asn for the point mutant hTNFR-1"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Arg Trp Lys Glu Phe Val Arg Arg Leu Gly Leu Ser Asp His Glu Ile
1               5                  10                  15

Asp Arg Leu Glu Leu Gln Asn Gly Arg Cys Leu Arg Glu Ala Gln Tyr
            20                  25                  30

Ser Met Leu Ala Thr Trp Arg Arg Arg Thr Pro Arg Arg Glu Ala Thr
        35                  40                  45

Leu Glu Leu Leu Gly Arg Val Leu Arg Asp Met Asp Leu Leu Gly Cys
    50                  55                  60

Leu Glu Asp Ile Glu Glu
65                  70
```

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 9 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala
1               5
```

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 6 amino acids
(B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Asp Thr Tyr Arg Tyr Ile
1 5

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 8 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Asp Tyr Lys Asp Asp Asp Asp Lys
1 5

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 117 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

AAGCCTGGTA CCATGCTGGG CATCTGGACC CTCCTACCTC TGGTTCTTAC GTCTGTTGCT 60

AGATTATCGT CCAAAGACTA CAAGGACGAC GATGACAAGA GTGTTAATGC CCAAGTC 117